

(1) GENERAL INFORMATION

- (2) INFORMATION FOR SEQ ID NO:1:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
1 5 10 15
Arg Pro Ala Pro
20

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGCTCCACCG CCCCCCAGC CCACGGTGTC ACCTCGGCCC CGGACACCAG GCCGGCCCCG 60

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Pro Asp Thr Arg Pro Ala Pro
1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGCAGTACTG CACCACCGGC ACATGGCGTA ACATCAGCAC CTGATACAAG ACCTGCACCT 60

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGATCCACCG CGCCGCTGCG GCACGGAGTG ACGTCGGCGC CCGACACGCG CCCCCTCCCC 60

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40536-0450P

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGGTCAACAG CTCCTCCCGC TCATGGGGTT ACTTCTGCTC CAGATACTCG CCCAGCTCCA 60

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGTTCGACGG CCCCCCTGC TCACGGTGTA ACATCCGCCC CGGATACCAG ACCGGCCCCCT 60

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGCAGCACCG CACGCCCCGC ACACGGGGTC ACAAGCGCGC CAGACACTCG ACCTGCGCCA 60

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGAAGTACCG CTCCACCTGC ACACGGGGTC ACAAGCGCGC CAGACACTCG ACCTGCGCCA 60

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGTCGACTG CCCCTCCGGC GCATGGTGTG ACCTCAGCTC CTGACACAAG GCCAGCCCCA 60

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(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGTTCAACGG CACCTCCAGC ACACGGAGTC ACGTCTGCAC CCGACACCCG TCCAGCTCCG 60

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGTAGTACAG CGCCACCCGC ACATGGCGTC ACGAGCGCTC CGGATACGAG ACCGGCGCCT 60

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGTCCACCG CACCCCCAGC CCACGGTGTC ACCTCGGCCC CGGACACCAG GCGGGCCCCG 60
GGTCCACCC CGGCCCCG 78

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGTCCACCG CCCCCCAGC CCATGGTGTC ACCTCGGCCC CGGACAACAG GCCCGCCTTG 60

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGCTCCACCG CCCCTCCAGT CCACAATGTC ACCTCGGCC

39

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Gly	Ser	Thr	Ala	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr
1				5			10						15	
Arg	Arg	Ala	Pro											
				20										

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Asn
1				5				10						15	
Arg	Pro	Ala	Leu												
				20											

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gly	Ser	Thr	Ala	Pro	Pro	Val	His	Asn	Val	Thr	Ser	Ala
1				5				10				

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40936-01500

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...1524
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATG ACA CCG GGC ACC CAG TCT CCT TTC TTC CTG CTG CTG CTC CTC ACA	48
Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Thr	
1 5 10 15	
GTG CTT ACA GCT ACC ACA GCC CCT AAA CCC GCA ACA GTT GTT ACG GGT	96
Val Leu Thr Ala Thr Thr Ala Pro Lys Pro Ala Thr Val Val Thr Gly	
20 25 30	
TCT GGT CAT GCA AGC TCT ACC CCA GGT GGA GAA AAG GAG ACT TCG GCT	144
Ser Gly His Ala Ser Ser Thr Pro Gly Gly Glu Lys Glu Thr Ser Ala	
35 40 45	
ACC CAG AGA AGT TCA GTG CCC AGC TCT ACT GAG AAG AAT GCT GTG AGT	192
Thr Gln Arg Ser Ser Val Pro Ser Ser Thr Glu Lys Asn Ala Val Ser	
50 55 60	
ATG ACA AGC TTG ATA TCG AAT TCC GGT GTC CGG GGC TCC ACC GCC CCC	240
Met Thr Ser Leu Ile Ser Asn Ser Gly Val Arg Gly Ser Thr Ala Pro	
65 70 75 80	
CCA GCC CAC GGT GTC ACC TCG GCC CCG GAC ACC AGG CCG GCC CCG GGC	288
Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly	
85 90 95	
TCC ACC GCC CCC CCA GCC CAC GGT GTC ACC TCG GCC CCG GAC ACC AGG	336
Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg	
100 105 110	
CCG GCC CCG GGC TCC ACC GCC CCC CCA GCC CAC GGT GTC ACC TCG GCC	384
Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala	
115 120 125	
CCG GAC ACC AGG CCG GCC CCG GGC TCC ACC GCA CCC CCA GCC CAC GGT	432
Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly	
130 135 140	
GTC ACC TCG GCC CCG GAC ACC AGG CGG GCC CCG GGC TCC ACC CCG GCC	480
Val Thr Ser Ala Pro Asp Thr Arg Arg Ala Pro Gly Ser Thr Pro Ala	
145 150 155 160	
CCG GGC TCC ACC GCC CCC CCA GCC CAC GGT GTC ACC TCG GCC CCG GAC	528
Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp	
165 170 175	
ACC AGG CCG GCC CCG GGC TCC ACC GCC CCC CCA GCC CAT GGT GTC ACC	576
Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr	
180 185 190	
TCG GCC CCG GAC AAC AGG CCC GCC TTG GGC TCC ACC GCC CCT CCA GTC	624
Ser Ala Pro Asp Asn Arg Pro Ala Leu Gly Ser Thr Ala Pro Pro Val	
195 200 205	

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CAC AAT GTC ACC TCG GCC TCA GGC TCT GCA TCA GGC TCA GCT TCT ACT	672
His Asn Val Thr Ser Ala Ser Gly Ser Ala Ser Gly Ser Ala Ser Thr	
210 215 220	
CTG GTG CAC AAC GGC ACC TCT GCC AGG GCT ACC ACA ACC CCA GCC AGC	720
Leu Val His Asn Gly Thr Ser Ala Arg Ala Thr Thr Thr Pro Ala Ser	
225 230 235 240	
AAG AGC ACT CCA TTC TCA ATT CCC AGC CAC CAC TCT GAT ACT CCT ACC	768
Lys Ser Thr Pro Phe Ser Ile Pro Ser His His Ser Asp Thr Pro Thr	
245 250 255	
ACC CTT GCC AGC CAT AGC ACC AAG ACT GAT GCC AGT AGC ACT CAC CAT	816
Thr Leu Ala Ser His Ser Thr Lys Thr Asp Ala Ser Ser Thr His His	
260 265 270	
AGC ACG GTA CCT CCT CTC ACC TCC TCC AAT CAC AGC ACT TCT CCC CAG	864
Ser Thr Val Pro Pro Leu Thr Ser Ser Asn His Ser Thr Ser Pro Gln	
275 280 285	
TTG TCT ACT GGG GTC TCT TTC TTT TTC CTG TCT TTT CAC ATT TCA AAC	912
Leu Ser Thr Gly Val Ser Phe Phe Phe Leu Ser Phe His Ile Ser Asn	
290 295 300	
CTC CAG TTT CCT TCC TCT CTC GAA GAT CCC AGC ACC GAC TAC TAC CAA	960
Leu Gln Phe Pro Ser Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln	
305 310 315 320	
GAG CTG CAG AGA GAC ATT TCT CAA ATG TTT TTG CAG ATT TAT AAA CAA	1008
Glu Leu Gln Arg Asp Ile Ser Gln Met Phe Leu Gln Ile Tyr Lys Gln	
325 330 335	
GGG GGT TTT CTG GGC CTC TCC AAT ATT AAG TTC AGG CCA GGA TCT GTG	1056
Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val	
340 345 350	
CTG GTA CAA TTG ACT CTG GCC TTC CGA GAA GGT ACC ATC AAT GTC CAC	1104
Leu Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His	
355 360 365	
GAC GTG GAG ACA CAG TTC AAT CAG TAT AAA ACG GAA GCA GCC TCT CGA	1152
Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg	
370 375 380	
TAT AAC CTG ACG ATC CCA GAC GTC AGC GTG AGT GAT GTG CCA TTT CCT	1200
Tyr Asn Leu Thr Ile Pro Asp Val Ser Val Ser Asp Val Pro Phe Pro	
385 390 395 400	
TTC TCT GCC CAG TCT GGG GCT GGG GTG CCA GGC TGG GGC ATC GCG CTG	1248
Phe Ser Ala Gln Ser Gly Ala Gly Val Pro Gly Trp Gly Ile Ala Leu	
405 410 415	
CTC CTG CTG GTC TGT GTT CTG GTT GCG CTG GCC ATT GTC TAT CTC ATT	1296
Leu Leu Leu Val Cys Val Leu Val Ala Leu Ala Ile Val Tyr Leu Ile	
420 425 430	
GCC TTG GCT GTC TGT CAG TGC CGC CGA AAG AAC TAC GGG CAG CTG GAC	1344
Ala Leu Ala Val Cys Gln Cys Arg Arg Lys Asn Tyr Gly Gln Leu Asp	
435 440 445	

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ATC TTT CCA GCC CGG GAT ACC TAC CAT CCT ATG AGC GAG TAC CCC ACC 1392
Ile Phe Pro Ala Arg Asp Thr Tyr His Pro Met Ser Glu Tyr Pro Thr
    450                455                460

TAC CAC ACC CAT GGG CGC TAT GTC CCC CCT AGC AGT ACC GAT CGT AGC 1440
Tyr His Thr His Gly Arg Tyr Val Pro Pro Ser Ser Thr Asp Arg Ser
    465                470                475                480

CCC TAT GAG AAG GTT TCT GCA GGT AAT GGT GGC AGC AGC CTC TCT TAC 1488
Pro Tyr Glu Lys Val Ser Ala Gly Asn Gly Gly Ser Ser Leu Ser Tyr
                485                490                495

ACA AAC CCA GCA GTG GCA GCC ACT TCT GCC AAC TTG TAG 1527
Thr Asn Pro Ala Val Ala Ala Thr Ser Ala Asn Leu
    500                505

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(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

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Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Thr
 1          5          10          15
Val Leu Thr Ala Thr Thr Ala Pro Lys Pro Ala Thr Val Val Thr Gly
    20          25          30
Ser Gly His Ala Ser Ser Thr Pro Gly Gly Glu Lys Glu Thr Ser Ala
    35          40          45
Thr Gln Arg Ser Ser Val Pro Ser Ser Thr Glu Lys Asn Ala Val Ser
    50          55          60
Met Thr Ser Leu Ile Ser Asn Ser Gly Val Arg Gly Ser Thr Ala Pro
    65          70          75          80
Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly
    85          90          95
Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg
    100          105          110
Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala
    115          120          125
Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly
    130          135          140
Val Thr Ser Ala Pro Asp Thr Arg Arg Ala Pro Gly Ser Thr Pro Ala
    145          150          155          160
Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp
    165          170          175
Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr
    180          185          190
Ser Ala Pro Asp Asn Arg Pro Ala Leu Gly Ser Thr Ala Pro Pro Val
    195          200          205
His Asn Val Thr Ser Ala Ser Gly Ser Ala Ser Gly Ser Ala Ser Thr
    210          215          220
Leu Val His Asn Gly Thr Ser Ala Arg Ala Thr Thr Thr Pro Ala Ser
    225          230          235          240
Lys Ser Thr Pro Phe Ser Ile Pro Ser His His Ser Asp Thr Pro Thr

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